

DR	EML1; Z30972; CGPPARN.
DR	PIR; S47489; S42469.
DR	HSSP; P10826; IHRA.
KW	RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
KW	NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
DNABIND	109 173 C4-TYPE ZINC FINGERS (TWO).
ZNFING	109 129 C4-TYPE.
ZNFING	146 168 C4-TYPE.
DOMAIN	288 475 LIGAND-BINDING (POTENTIAL).
SEQUENCE	475 AA; 54472 MW; 1146250 CN;
SQ	

- FUNCTION: RECEPTOR THAT BIND PROXOSOME PROLIFERATORS SUCH AS HYDROXYACIDS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR Binds TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-CoA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE PROXOSOMIC BETA-OXIDATION PATHWAY OF FATTY ACIDS.
- SUBCELLULAR LOCATION: NUCLEAR.
- SUBUNIT: HETERO-DIMER WITH THE RETINOID X RECEPTOR.
- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS

RESULT	PPAT 2	PPAT 3D	MOUSE	STANDARD;	PRT;	470 AA.
C	P31723;					
T	01-OCT-1994	(REL. 30,				
T	01-OCT-1994	CREATED)				
T	01-OCT-1994	(REL. 30,				
T	01-OCT-1994	LAST SEQUENCE UPDATE)				
D	01-OCT-1994	(REL. 30,				
E	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA					
N	PPARG,					
M	MUS MUSCULUS (MOUSE).					
S	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMATA;					

RECIPIENT ID PPTP_XENIA STANDARD; PRT; 477 AA.
 AC P37234;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-GAMMA).
 GN PPAR-G.

OS XENOPUS LAEVIS (AFRICAN CLAMED FROG)
OC EUDARVOTA; METIZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.

RN [1]
RN SEQUENCE FROM N.A.
RM 92191267
RA DREYER C., KREY G., KELLER H., GIVEL F., HELFTENBEIN G., WAHLI W.;
RL CELJ 68:879-887(1992).
RN [2]

RP

CHARACTERIZATION.

RM 94100165

RA KREY G., KELLER H., MAHFoudi A., MEDIN J., OZATO K., DREYER C.,
RA WAHLI W.;

BL J. STEROID BIOCHEM MOL BIOL. 47:65-73(1993).

CC -|-: FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.

CC -|-: SUBCELLULAR LOCATION: NUCLEAR.

CC -|-: TISSUE SPECIFICITY: EXPRESSED MAINLY IN ADIPOSE TISSUE AND KIDNEY.

CC -|-: DEVELOPMENTAL STAGE: ADULT.

CC -|-: SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC

CC NUCLEAR HORMONE RECEPTORS.

DR EMBL: MB8163; XLPARG.

DR PIR: C42214; C42214.

DR HSSP: P10826; IHR4.

DR TRANSFAC: T01354; -.

KW RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;

KW NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.

FT DNA BIND 113 177 C4-TYPE ZINC FINGERS (TWO).

FT ZN FING 113 133 C4-TYPE.

FT ZN FING 150 172 C4-TYPE.

FT DOMAIN 293 477 LIGAND-BINDING (POTENTIAL).

SQ SEQUENCE 477 AA; 54055 MW; 1113537 CN;

DB 6; Score 2579; Match 73.9%; QryMatch 71.4%; Pred. No. 0.00e+00;
Matches 357; Conservative 62; MisMatches 50; Indels 14; Gaps 10;

Db 1 iwdtempfwenlnfgnmnmnmasedhcopydkfpttvdfasins-hyddldketc 59

Db 20 MVDTEMPFWT-NFGCISSTDLSMHEHSISFDKPFPTVDFESSISTPHXEDI---PT- 73

Db 60 rndaspdydklqkqcqqsskkleppspfydkpq-oscakfedtpnsfiaievrgqd 118

Qy 74 RTDPWVADYDKLQKQCQQSSKKLEPPSPFYDKPQ-OSCAKFDTPNSFIAIEVRGCD 133

Db 119 kasqfhgvhacegckgfrrtriklylvercdlnerihkkserntcqffgkchavgm 178

Qy 134 KASGFHGVIAECGCKGEFFRTTRIKLYDRCRTRKRSRNCYCRCFKCLAVGM 193

Db 179 hnairformpoekkekkilaeessiddqlnpresaedqrvlakhlydysvkspltkakagh 238

Qy 194 HNAIREGRMPQAEKEKLLAETSSDTDQNPESADLRAKHYDYSITKSFPITRAKARI 253

Db 239 pdgfsrhqrnergytrhelaadggsgdgavre-praeagggsdnlpal-svalrg-qvr 294

Qy 254 LTKT-TDKSP-FVTDMSLNGEDEKTKFHTRPLQEQSKVEARTRIFGCCFRRTSEAVQ 311

Db 295 eitefaknpgfsldindqytllkyheifmtlaslmndqyivaegqgfmrreflk 354

Qy 312 EITEYAKSISGFYNLDINDQYTLLKYHEIYTMLASLMNDQYIVAEQGFMRREFLK 371

Db 355 slrkpsdmepkfafirnseleddsdlaifavillsgdrpgllnvkpledqsdll 414

OS XENOPUS LAEVIS (AFRICAN CLAMED FROG)
OC EUDARVOTA; METIZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.

RN [1]
RN SEQUENCE FROM N.A.
RM 92191267
RA DREYER C., KREY G., KELLER H., GIVEL F., HELFTENBEIN G., WAHLI W.;
RL CELJ 68:879-887(1992).
RN [2]

RP CHARACTERIZATION.

RM 94100165

RA KREY G., KELLER H., MAHFoudi A., MEDIN J., OZATO K., DREYER C.,
RA WAHLI W.;

BL J. STEROID BIOCHEM MOL BIOL. 47:65-73(1993).

CC -|-: FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.

CC -|-: SUBCELLULAR LOCATION: NUCLEAR.

CC -|-: TISSUE SPECIFICITY: EXPRESSED MAINLY IN ADIPOSE TISSUE AND KIDNEY.

CC -|-: DEVELOPMENTAL STAGE: ADULT.

CC -|-: SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC

CC NUCLEAR HORMONE RECEPTORS.

DR EMBL: MB8163; XLPARG.

DR PIR: C42214; C42214.

DR HSSP: P10826; IHR4.

DR TRANSFAC: T01354; -.

KW RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;

KW NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.

FT DNA BIND 113 177 C4-TYPE ZINC FINGERS (TWO).

FT ZN FING 113 133 C4-TYPE.

FT ZN FING 150 172 C4-TYPE.

FT DOMAIN 293 477 LIGAND-BINDING (POTENTIAL).

SQ SEQUENCE 477 AA; 54055 MW; 1113537 CN;

DB 6; Score 1946; Match 55.24%; QryMatch 53.8%; Pred. No. 0.00e+00;
Matches 247; Conservative 78; Mismatches 51; Indels 3; Gaps 3;

Db 92 espgal-niecricdgkdgasqhygvahcegckgfrrtrirklydkcdrcskiqkknr 150

Db 117 EEPNSLMAFECRVCGDKAASGFNYGHAEFGCKFRRRTTRIKLTYDRCNCRHKER 176

Qy 151 nkccyccrfhkslvksmgshairfgrmrprsekkakiaeiltchdiedsetadlkslakri 210

Db 177 NKCCYCFQKLVGSHNAIRGRPMQEKEKLAEI-SDIDQNPESADLRNALKH 235

Qy 211 yeajlknfmnmkvkarlsvgkssknppwindmelmaektlvakan-giqnkeve 269

Db 236 YDSVIKSFLPLTKARARLTYKTDRSPVTVDMNSLMMGEDKIKEKHITPLQEQSKVA 295

DB 6; Score 1946; Match 55.24%; QryMatch 53.8%; Pred. No. 0.00e+00;
Matches 247; Conservative 78; Mismatches 51; Indels 3; Gaps 3;

Db 92 espgal-niecricdgkdgasqhygvahcegckgfrrtrirklydkcdrcskiqkknr 150

Db 117 EEPNSLMAFECRVCGDKAASGFNYGHAEFGCKFRRRTTRIKLTYDRCNCRHKER 176

Qy 151 nkccyccrfhkslvksmgshairfgrmrprsekkakiaeiltchdiedsetadlkslakri 210

Db 177 NKCCYCFQKLVGSHNAIRGRPMQEKEKLAEI-SDIDQNPESADLRNALKH 235

Qy 236 YDSVIKSFLPLTKARARLTYKTDRSPVTVDMNSLMMGEDKIKEKHITPLQEQSKVA 295

Db	270 vrifhcqctsvetlelfakafanldndevtlykyveafamlssvmlndq 329 : : : : : : : : : : : : : : Qy 296 IRIFQCQFERSVAEQTETYKRSITPGVNLNDQVTLKYGVHEIYTMLASIMNRDG 355	
Db	330 mlvayngnffretfiklrlqkmdlfrgivtehqvlqvikk 449 : : : : : : : : : : : : : Qy 355 VLISEGGENTREFLKSRLRKPFCDNEPKPEPAVKENALELDSDIAFIATVILS GDRP 415	
Db	390 qlnvhgihkmgegivvlrlhqlqshpdditfphllqkmdlfrgivtehqvlqvikk 449 : : : : : : : : : : : : Qy 416 GLANVRPEDIQDNLQALELQLKLNAHPPESQFLAKRQMTDLRQIVTEHVQLQVIRK 475	
Db	450 tesaalhpilqeiyrdmy 468 : : : : : : : Qy 476 TETDMSLHPILQEYRDY 494	
RESULT	5	
ID	PPAR_MOUSE	STANDARD; PRT; 468 AA.
AC	P23204;	
DT	01-NOV-1991 (REL. 20, CREATED)	
DT	01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)	
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)	
DE	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA).	
GN	PPAR OR PPAR.	
OS	MUS MUSCULUS (MOUSE).	
OC	EUDERMIATA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RM	91015382	
DA	HEERMANN, J.	GREEN, S.
RL	NATURE 347:645-650 (1990)	
CC	- - FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.	
CC	- - SUBUNIT: HETERO-DIMER WITH THE RETINOID X RECEPTOR.	
CC	- - DISEASE: Peroxisome proliferators are a diverse group of chemicals that include hypolipidemic drugs, herbicides and industrial plasticizers. Administration of these chemicals to rodents results in the dramatic proliferation of hepatic peroxisomes as well as liver hyperplasia.	
CC	- - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, KIDNEY AND HEART, VERY WEAKLY EXPRESSED IN BRAIN AND TESTIS.	
CC	- - SIMILARITY: To other members of the steroid/thyroid/retinoid nuclear hormone receptors.	
CC	DR ENBL; X571638; MMPPAR. DR P11659; S11659. DR HSSP; P10826; ITRA. DR TRANSFAC; T00694; -.	
DR	PROSITE; PS00031; STEROID FINGER.	
KW	RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.	
FT	DNA BIND 102 166 C4-TYPE ZINC FINGERS (TWO).	
FT	ZN FING 102 122 C4-TYPE.	
FT	ZN FING 139 161 C4-TYPE.	
FT	DOMAIN 281 468 LIGAND-BINDING (POTENTIAL).	
SQ	SEQUENCE 468 AA; 52432 MW; 1094992 CR;	
DB	6; Score 1932; Match 64.6%; QryMatch 53.5%; Pred. No. 0.00e+00;	

	Matches 245; Conservative 79; Mismatches 53; Indels 2; Gaps 2;	US-08-380-051-2.rsp
Db	91 despsalnicericgdkgayhyvhacegckffrtirklrydkdcdrecksikqrk 150 : : : : : : : : : : : : : Qy 117 EEPNSLMSIAECRVCGDKASCFHYAHCEGCKFFRTTRKLIVDNCIRTHKSR 176	
Db	151 nkcpqrfrhlcokslsgmchnairgrmrsekkatkaeltdchdldsetadkslqkri 210 : : : : : : : : : : : Qy 177 NKQYCQRFQKCLAVGSHNAIRGRPQAEEKELAET-SSDIDQINPESADIRALKU 235	
Db	211 heaylknnfmnkvarkvlgaktsnppfrhdmelclmaektlvlakmvangved-kease 269 : : : : : : : : : : Qy 236 YDSVIKSFPLTKARLJLQKTYTDSPSPVYNSUMAGEDKIKTHPTLQEQSKVEA 295	
Db	270 vrfhccqcmasvetvielfakapgfandldindqftllkgyyeiaftmls1lmndq 329 : : : : : : : : : Qy 296 IRIFQGQFRSVEAQETTEYKASIPGFVNLDINDQVTLLKGHEIYTMLASLMNKDG 355	
Db	330 mliayngofitreflknlrpfdineptcfdfamknalelddsdsvltvaaiicgdrp 389 : : : : : : : : : Qy 356 VLISEGQGMMPREPKLSRCPFDMEPKPEFAVKAENALEDDSDIAFIAVILSGDRP 415	
Db	390 qllniqyeklqeqivhvlkhlsqnshpddtfifpkflqkmdvlrqvtehaqlqvikk 449 : : : : : : : : Qy 416 GLANKP1EDQDNLQALELQKLNHPSESSLFAKUQRMTDLRQIVTEHVQLQVTRK 475	
Db	450 tesdaalhpillqeiyrdmy 468 : : : : : : Qy 476 TETDMSLHPILQEYRDY 494	
RESULT	6	
ID	PPAR RAT	STANDARD; PRT; 468 AA.
AC	P37230;	
DT	01-OCT-1994 (REL. 30, CREATED)	
DT	01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)	
DT	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)	
DE	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA).	
GN	PPARA OR PPAR.	
OS	RATTUS NORVEGICUS (RAT).	
OC	EUROPIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RM	92264938	
RA	GOETTLICHER, M.; WIDMARK, E.; LI, Q.; GUSTAFSSON, J. A.;	
RL	PROC. NATL. ACAD. SCI. U.S.A. 89:4653-4657 (1992).	
CC	- - FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.	
CC	- - SUBCELLULAR LOCATION: NUCLEAR.	
CC	- - SIMILARITY: To other members of the steroid/thyroid/retinoid receptors.	
CC	CC NUCLEAR HORMONE RECEPTORS.	
DR	EMBL; M88592; RNPPAR.	
DR	P1B; A45288; A45288.	
DR	HSSP; P10826; ITRA.	
KW	RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.	
FT	DNA BIND 102 166 C4-TYPE ZINC FINGERS (TWO).	
FT	ZN FING 102 122 C4-TYPE.	
FT	ZN FING 139 161 C4-TYPE.	
FT	DOMAIN 281 468 LIGAND-BINDING (POTENTIAL).	
SQ	SEQUENCE 468 AA; 52432 MW; 1094992 CR;	
DB	6; Score 1932; Match 64.6%; QryMatch 53.5%; Pred. No. 0.00e+00;	

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US-08-380-051-2.rsp

11

US-08-380-051-2.rsp

12

CC	THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.	SEQUENCE FROM N. A. STRAIN=C57BL/6J; TISSUE=ADIPOCYTE; RC STRAIN=C57BL/6J; GRIMALDI P.; RA AMRI E.-Z.; BONINO F.; ALLAHD G.; GRIMALDI P.;
CC	-!- SUBCELLULAR LOCATION: NUCLEAR.	RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC	-!- SUBUNIT: HETERO-DIMER WITH THE RETINOID X RECEPTOR.	CC -!- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPO-LIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC	-!- TISSUE SPECIFICITY: UBIQUITOUS.	CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC	-!- DEVELOPMENTAL STAGE: OCYTES, EMBRYOS, AND ADULTS	CC -!- SUBUNIT: HETERO-DIMER WITH THE RETINOID X RECEPTOR.
CC	-!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS.	CC -!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS.
DR	EMBL; M84161; XLIPPARA.	DR EMBL; L28116; XLIPPARA.
DR	HSSP; P10826; IHRA.	DR HSSP; P10826; IHRA.
DR	PTR; A42214; A42214.	DR PROSITE; PS00031; STEROID FINGER.
DR	DR	DR RECEPTOR; TRANSCRIPTION ACTIVATOR; DNA-BINDING;
KW	RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.	KW RECEPTOR; TRANSCRIPTION ACTIVATOR; DNA-BINDING;
FT	DNA BIND 109 173 C4-TYPE ZINC FINGERS (TWO).	KW NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.
FT	DNA BIND 109 129 C4-TYPE.	FT DNA BIND 73 137 C4-TYPE ZINC FINGERS (TWO).
FT	ZN FING 146 168 C4-TYPE.	FT ZN FING 73 93 C4-TYPE.
FT	ZN FING 146 168 C4-TYPE.	FT ZN FING 110 132 C4-TYPE.
FT	DOMAIN 287 474 LIGAND-BINDING (POTENTIAL).	FT DOMAIN 253 440 LIGAND-BINDING (POTENTIAL).
SQ	SEQUENCE 474 AA; 52856 MW; 1122618 CN;	SQ SEQUENCE 440 AA; 49715 MW; 980155 CN;
DB 6;	Score 1894; Match 64.8%; QryMatch 52.4%; Pred. No. 0.00e+00; Matches 247; Conservative 74; Mismatches 56; Indels 4; Gaps 4;	DB 6; Score 1886; Match 63.6%; QryMatch 52.2%; Pred. No. 0.00e+00; Matches 241; Conservative 84; Mismatches 53; Indels 1; Gaps 1;
Db	97 aedacksl-nleevrdsksflasgfhvngahceckffrrtirkluyvdercermskdkh 155	Db 62 dgasegglnnmcrcvcdkasgfhvngahceckffrrtirrmleyekdrckiqkknr 121
Qy	115 PHEEPSNSLIAIECRVCGDKASGEHYGVHACECKGFRRTRIRKLITIDCDLNCRHKK 174	Qy 117 EEPNSNLMATECRVCGDKASGFHYGVHACEGCKGFRRTRIKLIMDNCRTHKSR 176
Db	156 srnkqcytcrcqkclavcmasnairfgrmpqaekekllakvaevlmdqdkvdksqadlls lar 215	Db 122 nkccpcrfqkclalgmshnairfgrmpqaekekllakvaevlmdqdkvdksqadlls khl 181
Qy	175 SRNKQCYTCRCQKCLAVCMASNAIRFGRMPQAEKEKLLAEI-SSDIDQINPESADIRALAKHL 233	Qy 177 NKCCQYCREQKCLAVGMASHNAIRGRPQAEKEKLLAEISSDD-QINPESADIRALAKHL 235
Db	216 liydaylknfnmkvkarilgtkasn-pfpvihdmelcmaektlvaklvan-qipke 273	Db 182 ynatylknfnmtkkarsiltgkshnapfvihdmelqatqkglvnglppyneis 241
Qy	224 HLYDYSYKSPPLTKAKARATLTGKTDKSPFVYDNLSMMGEDKIKFKHITPLQDQSKE 293	Qy 236 YDSYIKSEPLTKAKARATLTGKTDKSPFVYDNLSMMGEDKIKFKHITPLQDQSKEVA 295
Db	274 aervifhccgctevteltefaeksiqfteldldndqptllkygyteamfamlasvnk 333	Db 242 vhfvyrcgctevteltefaeksiqfteldldndqptllkygyteamfamlasvnk 301
Qy	294 VAIRIFQCCOFRSVEAQETEYAKATSIPEFVNIDANDQVTLKYGVHETTYMLASLANK 353	Qy 296 TRIFQCCOFRSVEAQETEYAKATSIPEFVNIDANDQVTLKYGVHETTYMLASLNRDG 355
Db	334 dgmlyvngqfitreflkslkrpkqdmptklefankfnalddsdalfraliced 393	Db 302 llvngsafvtheirlrkpsdilepkfekavfnalelldsdalffiaaiilcgdrp 361
Qy	354 DCVLISSEQFMREFLKSURKRFQDFMEPKFEFAVKENALELDSDAIFAVILSGD 413	Qy 356 VLISEGGQFMTRFLKSURKRFQDFMEPKFEFAVKENALELDSDAIFAVILSGDRP 415
Db	394 rpglmvpisiekqesivhrlkhlgsmhpddaf1fpkllqkmadrqlvrchaglvqtj 453	Db 362 glmavpypqveaqldtlrlakflhgvnphdqsglpkllqkmadrqlvrchaglvqtj 421
Qy	414 RPGLMVNPKIEDQDNLQLAEQIKLNHPESSQLFAKULLQRMTDLRQ1VTEHVLQQLVVI 473	Qy 416 GLIANKP1EDQDNLQLAEQIKLNHPESSQLFAKULLQRMTDLRQ1VTEHVLQQLVVI 475
Db	454 kttdalhplqeqiyrdny 474	Db 422 tesellhplqeqiyrdny 440
Qy	474 KKTETDMSLPLQEYKDL 494	Qy 476 GLIANKP1EDQDNLQLAEQIKLNHPESSQLFAKULLQRMTDLRQ1VTEHVLQQLVVI 494

RESULT	9	ID PP8 MOUSE STANDARD; PRT; 440 AA.
ID	P3396;	STANDARD;
AC	P3396;	PRT; 396 AA.
DT	01-JUN-1994 (REL. 29, CREATED)	DT P31233; STANDARD;
DT	01-OCT-1994 (REL. 29, LAST SEQUENCE UPDATE)	DT 01-OCT-1994 (REL. 30, CREATED)
DE	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA).	DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
GN	PPAR.	DE PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA).
OS	MUS MUSCULUS (MOUSE).	GN PPAR.
OC	EUDARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; RODENTIA.	
RN	[1]	

Db	471	9qv-mrdaiqmganarf--lvdstfnfaernmsmmltiaeiglfcailvltpdpjirn	527	Db	567	-ppccc-ah-llecoft- k -vs-amrh-grgplstp- c -hsglaapapelpqeqaf-	617
Qy	361	GQFMTRE-FLKSLRKPFGEDEMPKEFAVKENALEDDSDIAIFIAVILSGDRGHLN	419	Qy	243	FPLTKAKARAIILIGKTIDSPFVYDMNSLMEGEDIKIEKTHITPL-QEOSKEV-AIRFQ	300
Db	528	leiekmystlkqglcgviaqnpdpgeflakletmpdnlrlslhteklvfrtkeh	587	Db	618	s-q-rfahvirgvifqglqfqltlqdkftllkaglfdfalfrlicmfadsinsic	675
Qy	420	VRFIEDIQDNLQALEQTKLNHPESSQLFAKLQRMTDLRQIVTEHVQLQVIRKETD	479	Qy	301	GCQRSVEAQTETAYAKSIPGTVNLDDAQVTLKYKWHETIYTMLASIANKD-GVLIS	359
Db	588	1 588		Db	676	Ingv-mmrdaiqmganarf- lvdstfnfaernmsmmltiaeiglfcailvltpdpj	732
Qy	480	M 480		Qy	360	-EGGCFNTRE-FLKSLRKPFGEDEMPKEFAVKENALEDDSDIAIFIAVILSGDRGHL	417
RESULT	12			Db	733	rnlieiekmystlkqglcgviaqnpdpgeflakletmpdnlrlslhteklvfrtkeh	792
ID	E75C_DROME	STANDARD;	PRT;	Db	793	kel 795	
AC	P13055;			Qy	418	INVRPTEDIQDNLQALEQTKLNHPESSQLFAKLQRMTDLRQIVTEHVQLQVIRKETD	477
DT	01-JAN-1990	(REL. 13, CREATED)		DT	478	TDM 480	
DT	01-JAN-1990	(REL. 13, LAST SEQUENCE UPDATE)		Qy			
DT	01-OCT-1994	(REL. 30, LAST ANNOTATION UPDATE)		DB			
DE	ECDSONE-INDUCIBLE PROTEIN E75-C.			RESULT	13		
GN	E75B.			ID	PPAU_MOUSE	STANDARD;	PRT;
OS	DROSOPHILA MELANOGASTER (FRUIT FLY).			AC	P3739;		158 AA.
OC	EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA;			DT	01-OCT-1994	(REL. 30, CREATED)	
RN	[1]			DT	01-OCT-1994	(REL. 30, LAST SEQUENCE UPDATE)	
RP	SEQUENCE FROM N.A.			DT	01-OCT-1994	(REL. 30, LAST ANNOTATION UPDATE)	
RC	STRAIN=CANTON-S; TISSUE=HEAD;			DE	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR NUCL (PPAR-NUCL)		
RM	90016778			DE	(FRAGMENT).		
RA	FEIGL G., GRAM M., PONGS O.			OS	MUS MUSCULUS (MOUSE).		
RL	NUCLEIC ACIDS RES. 17:7167-7178 (1989).			OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
CC	- - FUNCTION: IMPLICATED IN THE REGULATION OF ECDSONE-TRIGGERED			OC	EUTHERIA; RODENTIA.		
CC	GENE HIERARCHIES. PROBABLY PLAYS A KEY ROLE IN MEDIATING THE			RN	[1]		
CC	REGULATION OF THE LARVAL MOLT BY 20-OH-ECDSONE.			RP	SEQUENCE FROM N.A.		
CC	- - SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).			RC	RC=BAIB/C; TISSUE=BRAIN/		
CC	- - INDUCTION: THE EXPRESSION OF THIS PROTEIN IS DEVELOPMENTALLY			RM	94059089		
CC	REGULATED AND IS CORRELATED WITH THE 20-OH-ECDSONE INDUCED			RA	CHEN F., LAW S.W., O'MALLEY B.R.;		
CC	ACTIVITY OF PUFF 75B.			RL	BIOCHEM. BIOPHYS. RES. COMMUN. 196:671-677(1993).		
CC	- - SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC			CC	-!- FUNCTION: RECEPTOR THAT BIND PEROXISOME SUCH AS		
CC	- - NUCLEAR HORMONE RECEPTORS.			CC	HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,		
CC	- - ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E75 ARE			CC	THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA		
CC	PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.			CC	OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE		
DR	PIRL, X15586; DM75B.			CC	PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.		
DR	HSSP; P10826; 1HRA.			CC	- - SUBCELLULAR LOCATION: NUCLEAR.		
DR	PIR; 505979; S5919.			CC	- - SUBUNIT: HETEROPTIMER WITH THE RETINOID X RECEPTOR.		
DR	FLYBASE; FBN0000568; EIP75B.			CC	- - SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC		
DR	PROSITE; PS00031; STEROID FINGER.			CC	NUCLEAR HORMONE RECEPTORS.		
KW	ZINC-FINGER; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;			DR	EMBL: U016665; MM665.		
KW	ZINC-FINGER; ALTERNATIVE SPLICING.			HSSP;	P10826; 1HRA.		
FT	DNA BIND	454	520	KW	RECEPTOR; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;		
FT	ZN FING	454	520	FT	NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY.		
FT	ZN FING	491	515	FT	ZN FING	86	150
SQ	SEQUENCE	1443	AA;	FT	C4-TYPE ZINC FINGERS (TWO).		
DB	2; Score	641;	Match 34.2%; QryMatch 17.7%; Pred. No. 9.62e-91;	FT	ZN FING	86	106
Matches	124;	Conservative	88;	FT	C4-TYPE.		
DB	451	tvlervegdasfhvghseckgfifrsiqliqrptknqcsilinrrcyc	510	FT	NON TER	123	145
Qy	125	AIEGRVCGDKASGEHYGVHAECEGGKFRRTRILKLYDRC-DLNCRHKSKRNKCYC	182	SQ	SEQUENCE	158	158
DB	511	rkkkciavgsndavrfgvpktrekariwpcnra-priaa-ssd-pappsm-tshass	566	SQ	158 AA;	17316 MW;	110700 CN;
Qy	183	RFONKCLAVGSHANAIRFGMPQAERKEKLAIEISSDQLNPESDAHLAKHLYDSYIKS	242	DB	6;	Score 558;	Match 77.4%; QryMatch 15.4%; Pred. No. 2.36e-75;
Matches	65;	Conservative	12;	DB	Matches 65;	Mismatches 7;	Indels 0;
DB	75	EEPSNSLMATECRVCGDKASGFHYGVHAECEGGKFRRTRILKLYDRC-DLNCRHKSKRNKCYC	134	Qy	117		Gaps 0;

Db	135	nkccyprfqccelgashairfg	158	
		: : : :		
Qy	177	NKQYCRFQRCLAVGASHNARFG	200	
RESULT	14			
ID	E7B DRONE	STANDARD;	PRT;	1394 AA.
AC	P1672;			
DT	01-AUG-1990 (REL. 15, CREATED)			
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)			
DT	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)			
DE	ECDSONE-INDUCIBLE PROTEIN E75-B.			
GN	E1P75B.			
OS	DROSOPHILA MELANOGASTER (FRUIT FLY).			
OC	EDAROTYA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CANTON-S;			
RA	90249127			
RA	SERGAEWS W.A., HOGNESS D.S.;			
RL	GENES DEV. 4: 204-219 (1990).			
CC	- - FUNCTION: IMPLICATED IN THE REGULATION OF ECDSONE-TRIGGERED GENE HIERARCHIES. PROBABLY PLAYS A KEY ROLE IN MEDIATING THE REGULATION OF THE LARVAL MOLT BY 20-OH-ECDSONE.			
CC	- - SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).			
CC	- - INDUCTION: THE EXPRESSION OF THIS PROTEIN IS DEVELOPMENTALLY REGULATED AND IS CORRELATED WITH THE 20-OH-ECDSONE INDUCED ACTIVITY OF PUFF 75B.			
CC	- - SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS BUT LACK THE DNA-BINDING REGION.			
CC	- - ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E75 ARE PROBABLY PRODUCED BY ALTERNATIVE SPlicing OF THE SAME GENE.			
DR	EMBL; X51549; DME75B.			
DR	PIR; B34598; B34598.			
DR	HSSP; P10826; IHRA.			
DR	TRANSFAC; T01368; -.			
DR	FLYBASE; FBGN000568; EIP75B.			
KW	RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;			
KW	ZINC-FINGER; ALTERNATIVE SPlicing.			
SQ	SEQUENCE 1394 AA; 152097 MW; 9605497 CN;			
DB	2; Score 528; Match 30.4%; QryMatch 14.6%; Pred. No. 7.64e-70; Matches 105; Conservative 90; Mismatches 131; Indels 19; Gaps 17;			
Db	415 avtanedadffrsiqiqhqrptckngqcsilinrrnrcycklkkciavgnrsadrav 474 : :			

Db	701	yivgnrpdpofekletcpdflstltkekfrtchel	745	
Qy	436	LQKLUNHPESSLQAKLQLQMTDLRQIVTEHVOLLQVIKKTETDM	480	
RESULT	15			
ID	THB1_XENLA	STANDARD;	PRT;	369 AA.
AC	P1816;			
DT	01-Nov-1990 (REL. 16, CREATED)			
DT	01-Nov-1990 (REL. 16, LAST SEQUENCE UPDATE)			
DT	01-Oct-1994 (REL. 30, LAST ANNOTATION UPDATE)			
DE	THYROID HORMONE RECEPTOR BEta-1.			
OS	XENOPUS LAEVIS (AFRICAN CLAMED FROG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RM	90384953			
RA	YAOITA Y., SHI Y.-B., BROWN D.D.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:7090-7094 (1990).			
RN	[2]			
ERRATUM.				
RM	91046059			
RA	YAOITA Y., SHI Y.-B., BROWN D.D.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:8684-8684 (1990).			
CC	- - FUNCTION: HIGH AFFINITY RECEPTOR FOR TRIIODOTHYRONINE.			
CC	- - SUBCELLULAR LOCATION: NUCLEAR.			
CC	- - DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.			
CC	- - SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS.			
CC	- - ALTERNATIVE PRODUCTS: SPLICING OF THE BETA-1 GENE PRODUCES VARIANTS OF THE RECEPTOR.			
DR	EMBL; M35359; XLBETA.			
DR	PIR; C36067; C36067.			
DR	HSSP; P10826; IHRA.			
KW	PROSITE; PS00031; STEROID FINGER.			
KW	RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER; MULTIGENE FAMILY; ALTERNATIVE SPlicing.			
FT	DOMAIN 1	14	MODULATING (POTENTIAL).	
FT	DNA BIND	15	82	C4-TYPE ZINC FINGERS (TMQ).
FT	ZN FING	15	35	C4-TYPE.
FT	ZN FING	53	77	C4-TYPE.
FT	DOMAIN	132	369	LIGAND-BINDING.
SQ	SEQUENCE	369 AA;	41939 MW;	691170 CN;
DB	7;	Score 525;	Match 31.4%;	QryMatch 14.5%;
Matches	117;	Conservative 99;	Mismatches 131;	Indels 26;
Gaps	25;			
DB	15	cvcgdkatgghyrctieqckoffrttkqnlhpssckyekvckdvtvrnqcgcrf	74	
Qy	128	CRVCGDRASGFHYRCECKGFFRRTIKLRRDK-RCDCNICHRSRNKCOYCRF	184	
DB	75	kkciavgmataolv-lddnkklakrkiee-nre-krkrke-de-iq-kalvqkp-eptcqewe	128	
Qy	245	LTAKARAILTGTQKTPDKSPFVTDMSLAMGKD-VYLIS-EQGMFTRE-FIKSLRK	375	
DB	129	liqvteahvtnaqg-shw-k-qkrfkfl-ped-igqapivnaeqgk-vdleaf-s-qf	180	
Qy	319	SIFGFVNLDINDQVTLKYGHELIYTMILASIMND-GVLLS-ECQGMFTRE-FIKSLRK	304	
DB	181	tkittpairvdakklnpfcelpqdlkllgcaiflglrlneileknysrlkgclq	700	
Qy	376	mpqqlttqdkftllkgafldlfalvrlcmfdssnlciiclnqgna 642	239	
Qy	319	SIFGFVNLDINDQVTLKYGHELIYTMILASIMND-GVLLS-ECQGMFTRE-FIKSLRK	304	
DB	181	rf--lvdstfnfaermsmltadieglcailvlitpdpgrlnrlleiknytsglq	700	
Qy	376	PFGDFMPKEFAVKFNALLEDDSDIAIFIATVLSGORGFLUNTKPTEIDQNLLQALE	435	
Qy	305	-RSVE-AVQEITEVAKSIPGVNLINDQVTLKYGHELIYTMILASIMND-NRDG-VLISE	360	

Nov 17 08:25

US-08-001-2.rp 19

Db 240 gematrqqikn--gg!gvrsdaifdgvslssfdtevalgavilmassdrpglasv 297
 |: ::|| |::| :| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Qy 361 GQGEMTREFIKSLSRKPGDFMEPKFEFAVKFNALEDDSDAIFAVILSDRFLGIANV 420
Db 298 eriekcegfilafelafehiynrkmiahfpkklmkvtldrmiigachasrfilmhkcepte 357
 || |: ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Qy 421 KPIEDIQNLLQALEQIKLNHPESSQLEPAKLIQMTDLRQIVTEHV-QLQVIKKTED 479
Db 358 1-fpp1flverfed 369
 : :||: |::|
Qy 480 MSLHPLIQLQEYKD 492

Search completed: Fri Nov 17 08:30:52 1995
Job time : 15 secs.

DB 10;	Score 3454;	Match 97.3%;	QryMatch 95.6%;	Pred. No. 0.00e+00;	
Matches 469;	Conservative 11;	Mismatches 2;	Indels 0;	Gaps 0;	
Db 24 stseqitmvatempfwptnqfgesvdlsmedishsfdfikpfttvdessisaphyedipf 83					Qy 20 MVDTEMPFWPTNQFGESVDLSMEDISHSFDFIKPFTTVDSSISAPHYEDIPFTDPPV 79
Qy 13 SAFNEMTMVDTMPFWPTNQFGESVDLSMEDISHSFDFIKPFTTVDSSISAPHYEDIPF 72					
Db 84 traqpavdckydklqeyesaikvepasppyysektqllynphheepsnsImaiecrvcgdkasgfh 143					Db 61 adkydklqeydsalkvepasppyysektqllynphheepsnsImaiecrvcgdkasgfh 120
Qy 73 TRDPWVADYDILKLEQEYOSAIKEPVASPPYYSEKTQLYNKPHEEPNSNLMATECRVCG 132					Qy 80 ADKYDKLQEQYOSAIKEPVASPPYYSEKTQLYNKPHEEPNSNLMATECRVCGDKASGFH 139
Db 144 dkasgfhgyvhacegchgffrrirkllydrdncrihkhkrrkccyccrfqkclavgm 203					Db 121 yvhacegckgffrrirkllydrdncrihkhkrrkccyccrfqkclavgmshnairf 180
Qy 133 DKASGFHYGHACEGCKGFFRIRKLLYDRDNCRHKSRHKCQYCREQKCLAVGM 192					Qy 140 YGHACECSCKFFRTIRKLLYDRCDLNCRHKSRHKCQYCREQKCLAVGMSHNAIRF 199
Db 204 shnaifgrmpqaekeklaiesiddqdlnpesadr.alakh.lysyksfpktakara 263					Db 181 qmpqaekhlaiesiddqdlnpeasdralakh.lydayiksfpktakaraltgttt 240
Qy 193 SHNAIFGRMPQAEKEKLLAIESDDQDINPESADR.ALAKH.LYSYKSFPPLTKAKARA 252					Qy 200 GRMPQAEEKEKLLAIESDDQDINPESADR.ALAKH.LYSYKSFPPLTKAKARLTGTIT 259
Db 264 iltgkttdkpkfrvijdmnslmqgedkikfkhplqeqskevairifqfcqfrsveavqe 323					Db 241 dkspfvijdmnslmqgedkikfkhplqeqskevairifqfcqfrsveavqeiteyakn 300
Qy 253 ILTGKTTDKPKFRVJDMNSLMQGEDKIKFKHPLQEQSKEVAIRIFQFCQFRSVEAVQE 312					Qy 260 DKSPEVYDANSIQLMGGEDKIKFKHPLQEQSKEVAIRIFQFCQFRSVEAVQEITEYAKS 319
Db 324 iteyaknijpgfinldndqvtllkygheiytm.laslmkdgvliqeqfmtrfe.fkn 383					Db 301 ipgfinldndqvtllkygheiytm.laslmkdgvliqeqfmtrfe.fkn 360
Qy 313 ITEYAKNIPGFVNLDNDQVTLLKYGHEITYTM.LASLMKDGVLIQEQQGFMTRFEFLKS 372					Qy 320 IPGFVNLDNDQVTLLKYGHEITYTM.LASLMKDGVLIQEQQGFMTRFEFLKS.LRKPFQD 379
Db 384 lrkpfgdffmepkfefavknaleldsdlaifavilsgdrpgl1nvypiediqdnllq 443					Db 361 fmepkfefavknaleldsdlaifavilsgdrpgl1nvypiediqdnllqalefqk 420
Qy 373 LRKEFGDFMPEKFEPFKNALEDDSDLAIFAVILSGDRPGL1NVYPIEDIQDNLLQ 432					Qy 380 FMEPKFEFAVKFNALEDDSLAIFAVILSGDRPGL1NVYPIEDIQDNLLQALEDQK 439
Db 444 aleqlklnphesqifakyjqlqntdlrqiivtehvgllhvikktecdmslhp1lqeiyk 503					Db 421 Inhpesqlfakvlqkmtdlrqiivtehvgllhvikktecdmslhp1lqeiykdy 475
Qy 433 ALEQLKLNPHESQIFAKVJQLQNTDLRQIVTEHVGLLHVIKKTEDMSLHP1LQEIYKD 492					Qy 440 INHPESSOPLAKLQMTDLRQIVTEHVGLLQVKKTEDMSLHP1LQEIYKD 494
RESULT 2	A49294	#type complete			RESULT 3
ENTRY		peroxisome proliferator-activated receptor gamma - mouse			ENTRY S42489 #type complete
TITLE		#formal_name Mus musculus #common_name mouse			TITLE Peroxisome proliferator activated receptor - human
ORGANISM		#sequence_revision 19-May-1995 #text_change			ORGANISM #formal_name Homo sapiens #common_name man
DATE		19-May-1995 #sequence_revision 06-Jan-1995 #text_change			DATE 06-Jan-1995
ACCESSIONS					ACCESSIONS S42489
REFERENCE					REFERENCE Aperlo, C.; Pogonec, P.; Auwerx, J.; Boulikos, K.
A49294					#status preliminary
A49294					#molecule_type mRNA
Authors Zhu, Y.; Alvarez, K.; Huang, Q.; Rao, M.S.; Reddy, J.K.					#residues 1-475 #label APE
Journal J. Biol. Chem. (1993) 268:26817-26820					#cross-references EMBL:239972
Title Cloning of a new member of the peroxisome					#length 475 #molecular-weight 54472 #checksum 5251
proliferator-activated receptor gene family from mouse					SUMMARY
liver.					DB 10; Score 3433; Match 97.1%; QryMatch 95.0%; Pred. No. 0.00e+00; Matches 464; Mismatches 11; Indels 0; Gaps 0;
#status preliminary					Db 1 mvdtempfwptnqfgesvdlsmedishsfdfikpfttvdssisaphyedipftadpmv 60
#molecule_type mRNA					Qy 20 MVDTEMPFWPTNQFGESVDLSMEDISHSFDFIKPFTTVDSSISAPHYEDIPFTDPPV 79
#residues 1-475 #label ZHU					Db 61 adkydklqeydsalkvepasppyysektqllynphheepsnsImaiecrvcgdkasgfh 120
#cross-references GB:U01841					Qy 80 ADKYDKLQEQYOSAIKEPVASPPYYSEKTQLYNKPHEEPNSNLMATECRVCGDKASGFH 139
SUMMARY #length 475 #molecular-weight 54511 #checksum 6045					Db 121 yvhacegckgffrrirkllydrdncrihkhkrrkccyccrfqkclavgmshnairf 180
DB 10;	Score 3439;	Match 98.1%;	QryMatch 95.2%;	Pred. No. 0.00e+00;	
Matches 466;	Conservative 9;	Mismatches 0;	Indels 0;	Gaps 0;	
Db 1 mvdtempfwptnqfgesvdlsmedishsfdfikpfttvdssisaphyedipftadpmv 60					

Nov 17 08:26

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5

US-08-380-051-2.rpt

Nov 17 08:26

Qy 140 YGVHACECGEGFFFRTRIKLYTYRCDLNCRHKSRNSRCYCRCRKCLAGMSHNAIRF 199
 Db 181 gmpqaekekllaaeissddiqlnpesadrlalakhlydysksfpftkakaraltgttt 240
 Qy 200 GRMPQAEEKEKLLAEISSDDIQLNPESSADRLALAKHLYDYSKSFPLTKAKARALTGT 259
 Db 241 dkspfviydnasfmmgedkikfkhitcplqeqskevairifqgqfrsveaqteyakn 300
 Qy 260 DKSPFVYDNASLMMGEDKIKFKHITCPLQEQSKEVAIRIFQGQFSSVEAQTEYAKS 319
 Db 301 ipgfinldndqvtlikyghetiyctalasmkdgvliseeggfntreflklsrkfcd 360
 Qy 320 IPGFVNDLNDQVTLKLYGHETIYTMLASLANKDGLISEGGPFTRFLKSJRKPGD 379
 Db 361 fmepkfefavkfnalelddsdlafiaiilslqaldqnlqalelk 415
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 Qy 380 FMEPKFEFAKFLAELDDSDLAIFIATIVLSDRGLANVKPIDIQDNLQLALELK 439
 Db 416 Inhpeseqtlakvjqkntdirqivtbehqlhvikkterdmshp1qeykdly 470
 Db 421 Inhpeseqtlakvjqkntdirqivtbehqlhvikkterdmshp1qeykdly 475
 Qy 440 LNHFESSQLEFKLJQKMTDLRQIVTETHVQLQVKKTETDMSLHPLQEIYKDY 494

RESULT 4 JN0881 #type complete
 ENTRY TITLE peroxisome proliferator activated receptor gamma precursor -
 ORGANISM mouse #formal_name Mus musculus #common_name house mouse
 DATE 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
 03-Mar-1995
 ACCESSIONS C42214
 REFERENCE JN0881
 #authors Chen, F.; Lau, S.W.; O'Malley, B.W.
 #journal Biochem. Biophys. Res. Commun. (1993) 196:671-677
 #title Identification of two mPPAR related receptors and evidence
 for the existence of five subfamily members.
 #accession JN0881
 #molecule_type mRNA
 #residues 1-470 #label CHE
 #experimental_source heart
 CLASSIFICATION #superfamily erba transforming protein homology
 KEYWORDS DNA binding
 FEATURE 1-22
 23-470 #domain signal sequence #status predicted #label SIG
 #product peroxisome proliferator activated receptor
 Gamma #status predicted #label MAT
 #domain erba transforming protein homology #label ERBA
 SUMMARY #region DNA-binding
 #length 470 #molecular-weight 54014 #checksum 9480

DB 10; Score 331; Match 96.2%; QryMatch 91.6%; Pred. No. 0.00e+00;
 Matches 457; Conservative 11; Mismatches 2; Indels 5; Gaps 1;

Db 1 mvdttempfwpt-nfgci5svdls/menidhsfdikpftvdess1spphyedi--pft- 73
 130-194
 Qy 20 MVDTTEMPFWPT-NFGCI5SVDLS/MENIDHSFDIKPFTVDESS1SPPHYEDIPTRTDPV 79

Db 61 adydklkgqeygsaitvepasppyysektqllynprheepsnslmiaeercvgdksagfh 120
 80 ADYDKLKGQEYGSAITVEPASPPYYSEKTQLYNPRHEEPSNSLMIAEERCVGDKASGFH 139
 Db 121 yghacecgfgrtrirklytqasrkverpasppyysektqllynprheepsnslmiaeercvgdksagfh 180

Qy 140 YGVHACECGEGFFFRTRIKLYTYRCDLNCRHKSRNSRCYCRCRKCLAGMSHNAIRF 199
 Db 181 grdrqaekekllaaeissddiqlnpesadrlalakhlydysksfpftkakaraltgttt 240
 Qy 200 GRMPQAEEKEKLLAEISSDDIQLNPESSADRLALAKHLYDYSKSFPLTKAKARALTGT 259
 Db 241 dkspfviydnasfmmgedkikfkhitcplqeqskevairifqgqfrsveaqteyakn 300
 Qy 260 DKSPFVYDNASLMMGEDKIKFKHITCPLQEQSKEVAIRIFQGQFSSVEAQTEYAKS 319
 Db 301 ipgfinldndqvtlikyghetiyctalasmkdgvliseggfntreflklsrkfcd 360
 Qy 320 IPGFVNDLNDQVTLKLYGHETIYTMLASLANKDGLISEGGPFTRFLKSJRKPGD 379
 Db 361 fmepkfefavkfnalelddsdlafiaiilslqaldqnlqalelk 415
 Qy 380 FMEPKFEFAKFLAELDDSDLAIFIATIVLSDRGLANVKPIDIQDNLQLALELK 439
 Db 416 Inhpeseqtlakvjqkntdirqivtbehqlhvikkterdmshp1qeykdly 470
 Db 421 Inhpeseqtlakvjqkntdirqivtbehqlhvikkterdmshp1qeykdly 475
 Qy 440 LNHFESSQLEFKLJQKMTDLRQIVTETHVQLQVKKTETDMSLHPLQEIYKDY 494

RESULT 5 C42214 #type complete
 ENTRY TITLE peroxisome proliferator-activated receptor gamma,
 ORGANISM xPARgamma-a nuclear receptor - African clawed frog
 #formal_name Xenopus laevis #common_name African clawed frog
 DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
 04-Mar-1993
 ACCESSIONS C42214
 REFERENCE A42214
 #authors Dreier, C.; Krey, G.; Keller, H.; Givel, F.; Heifzenbein, G.;
 Wahli, W.
 #journal Cell (1992) 68:879-887
 #title Control of the peroxisomal beta-oxidation pathway by a novel
 family of nuclear hormone receptors.
 #cross-references MUID:92191267
 #cross-references accession C42214
 #status preliminary; not compared with conceptual translation
 #molecule_type nucleic acid
 #residues 1-477 #label DRE
 #cross-references NCBI:88295
 #note sequence extracted from NCBI backbone
 SUMMARY #length 477 #molecular-weight 54055 #checksum 68550
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 #product peroxisome proliferator activated receptor
 Gamma #status predicted #label MAT
 #domain erba transforming protein homology #label ERBA
 #region DNA-binding
 FEATURE 1-22
 23-470 #domain signal sequence #status predicted #label SIG
 #product peroxisome proliferator activated receptor
 Gamma #status predicted #label MAT
 #domain erba transforming protein homology #label ERBA
 SUMMARY #region DNA-binding
 #length 470 #molecular-weight 54014 #checksum 9480

DB 9; Score 2579; Match 73.9%; QryMatch 71.4%; Pred. No. 0.00e+00;
 Matches 357; Conservative 62; Mismatches 50; Indels 14; Gaps 10;

Db 1 mvdttempfwpt-nfgci5svdls/menidhsfdikpftvdess1spphyedi--pft- 73
 Qy 20 MVDTTEMPFWPT-NFGCI5SVDLS/MENIDHSFDIKPFTVDESS1SPPHYEDI--PFT- 73

Db 60 rndqspidkydklqeqcisskleppspfydkpg-cskafedtpnsfiaeercvgd 118
 Qy 74 RTDPVWYDVKDJKLQEQYQSARVERPASPPYYSEKTQLYNPRHEEPSNSLMATEVCDD 133

Db 119 kasgfhugvhacecgfgrtrirklytqasrkverpasppyysektqllynprheepsnslmiaeercvgdksagfh 178
 Qy 134 KASGFHYCVHACECGFGRTRIKLYTQASRKVERPASPPYYSEKTQLYNPRHEEPSNSLMATEVCDD 193

Db 179 hnafgrmpaaetekllaaeissddiqlnpesadrlalakhlydysksfpftkakapgh 238
 Qy 194 HNAIRERGMPPDAEKEKLLAEISDDIQLNPESSADRLALAKHLYDTSKSPFLTKAKARAI 253

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Db	239	pdgqrhsqrsgytrheldaddggdsdqgavre-praegggdsnlpal-svalrg-qvr	294
Yq	254	LTEKT-TEKSP-FVYDMSLAMGDKTUKFTRUPLQEQSKERAVRIFQGQFRSEVAQO	311
Db	295	eitefaknipgfvslldndqrllykgheiiifmlaslmpkdgylvaeggftmreflk	354
Yq	312	EITEYAKSPGPFWNLINQVTLKYGVHEIITYTMALASLMRDGVWLSGEQGMFTRFLK	371
Db	355	sirkpfdmepkpfefairfnseleddsdlaifavvailsgdrpgllnvkpiediqsdl	414
Yq	372	SIRKPKDPMEPKPFEPAVEKFNALELDSDLAFTAVTILSCKRPGLLNKVPEDIQNUL	431
Db	415	qaleqlqklnhpdsadqafaklqkmtdlrrqvtvhqvlqlqikteadmcilhpqllceiyk	474
Yq	432	QALEQLQKLNHPDSSQFLAKLQKMDLQRQIVTENVQJQVTKETOMSLHPQJQEYK	491
Db	475	dly	477
Yq	492	DLY	494
RESULT	6		
ENTRY	A49289	#type complete	
TITLE		peroxisome proliferator-activated receptor - human	
ORGANISM		#formal name Homo sapiens #common name man	
DATE	07-Apr-1994	#sequence_revision 07-Apr-1994 #text_change	
07-Apr-1994			
ACCESSIONS			
REFERENCE	A19289		
authors	Sher, T.; Yi, H.F.; McBride, O.W.; Gonzalez, F.J.		
journal	Biochemistry (1993) 32: 5538-5604		
title	cDNA cloning, chromosomal mapping, and functional characterization of the human peroxisome proliferator activated receptor.		
accession	A49289		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-468	#label SHE	
#cross-references	GB:1:02932		
#note	authors translated the codon AAC for residue 33 as As		
GENETICS			
#map_position	22		
SUMMARY			
DB 10;	Score 1946;	Match 65.2%; OryMatch 53.8%; Pred. No. 3.90e-25	
Matches 247;	Conservative 78;	Mismatches 54; Indels 3; Gaps	
Db	92	espgal-niecricdkqasgphyghnacegkgfirrtirklyvdrcskqhknn 150	
Yq	117	EEPSNSLMAIECRVCGDDKASGFHYGPHAGEGKGFFRRTIRKLKYIDRCINCRHKRSR	176
Db	151	nikecfrfhkclsvqmsahairfgmpseakkhailetcldedsetadkslakri	210
Yq	177	NKCQICRFORCLAVGNSHAIREFGRPQAREKELIAE-SDIDQIAPESADRLAHLK	235
Db	211	yeaylknfmrnkvakrlsksasgashmpfvrldmetlmaeltlvaklvan-giqnkeve	269
Yq	236	YDSYIKSFPLTRAKARALIGKTDKSPVITIDMSLAMGEKIKFKHTLPQESKEVA	295
Db	270	vrifhccqctsvetvtelrefakapafanldndvttlkkygyeaifamlssymtdq	329
Yq	296	IRIFQGQFSRVEAOEYEYAKSIPGFTNLDINDQVTLKVGHEIYTMLASLANKDQ	355

Db	330	mlrayngfitreflkisrkpcdimepktdfamknalelddesidlfraiaicgdrp 389	
Qy	356	VLSSEGCGTREFLKISRKPCDFMEPKCFEVKFNALEDDSDAIFAVILSGDRP 415	
Db	390	qllnqhiemqeqivhvlhlqsnhpddiflpklqlqmadrqlvtehqvlqvikk 449	
Qy	416	GLANRPIEONIQLQALEQIQLKLNHPESSQLFAKUQRMIDLRQIVTEHVQLQVIKK 475	
Db	450	tesdaalhpqlqeyrdmy 468	
Qy	476	TEDMSLHPQLQEYRDY 494	
RESULT	7	S11659	# type complete
ENTRY			peroxisome proliferator-activated receptor - mouse
TITLE			formal name <i>Mus musculus</i> #common_name house mouse
ORGANISM			#sequence_revision 13-Jan-1995 #text_change
DATE			13-Jan-1995
ACCESSIONS		S11659	
REFERENCE		S11659	
#authors		Iissemann, I.; Green, S.	
#journal		Nature (1990) 347: 645-650	
#title		Activation of a member of the steroid hormone receptor superfamily by peroxisome proliferators.	
#cross-references		MUID:9105382	
#accession		S11659	
#status		Preliminary	
#molecule_type		mRNA	
#residues		1-468	#label ISS
SUMMARY		# length 468	#molecular_weight 52432 # checksum 4196
DB 10;	Score	1932;	Match 64.6%; QryMatch 53.5%; Pred. No. 4.42e-25
Matches	245;	Conservative 79; Mismatches 53; Indels 2; Gaps	
Db	91	despgsalniecrgdkasghyvhgahcegckoffrrtlklyvdckdrscslqknnr 150	
Qy	117	EEPSNSLMAECRVGDKASGFHYVHACGCGFFRTLKLIVDCLNCHHKRSR 176	
Db	151	nkgycyrcfhclevgmshnairgrpmorsekkakkaeltcehdksedatdklskgri 210	
Qy	177	NKQCYCRFCKLAVGSHNARIRGRPMQAEKXLAEL-SSDQLNPESADJRLAKHL 235	
Db	211	heavylknfmnkkyarvalqktssnpoppvhdmelcnmaektlvkavmvangved-keae 269	
Qy	236	YDSTKSPFLTKAKARLTGKTIDKSPEVYDNLSMGMGEDKIKFKEHTPLQDQSEKEVA 295	
Db	270	vrffhccqcmstvteltefakaipofanldindvptllyguyyeaiftmlslnmkdg 329	
Qy	296	TRIFQGQFERSVEAQETTYSKARSTIPFVNLDANDQVTLKYGVHEITYMLASLMRKDG 355	
Db	330	mlrayngfitreflkisrkpcdimepktdfamknalelddesidlfraiaicgdrp 389	
Qy	356	VLSSEGCGTREFLKISRKPCDFMEPKCFEVKFNALEDDSDAIFAVILSGDRP 415	
Db	390	qllnqhiemqeqivhvlhlqsnhpddiflpklqlqmadrqlvtehqvlqvikk 449	
Qy	416	GLANRPIEONIQLQALEQIQLKLNHPESSQLFAKUQRMIDLRQIVTEHVQLQVIKK 475	
Db	450	tesdaalhpqlqeyrdmy 468	
Qy	476	TEDMSLHPQLQEYRDY 494	

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RESULT 8 JC2085 #type complete
 ENTRY proliferator activated receptor alpha chain - mouse
 TITLE #formal name Mus musculus #common name house mouse
 ORGANISM 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
 DATE 14-Jul-1994
 ACCESSIONS JC2085
 REFERENCE Gearing, K.L.; Crickmore, A.; Gustafsson, J.A.
 AUTHORS Biochem. Biophys. Res. Commun. (1994) 199:255-263
 JOURNAL Structure of the mouse peroxisome proliferator activated
 TITLE receptor alpha gene.
 #accession JC2085
 #molecule_type DNA
 #residues 1-468 #label GEA
 #cross-references EMBL:X75287; EMBL:X75288; EMBL:X75289; EMBL:X75290;
 EMBL:X75291; EMBL:X75292; EMBL:X75293
 COMMENT This protein mediates transcription of responsive genes which
 include those encoding peroxisomal enzymes and members of the
 cytochrome P450 family of drug metabolising enzymes.
 GENETICS
 #gene PPAlpha
 #introns 70/1; 123/2; 170/1; 237/3; 387/1
 KEYWORDS DNA binding; receptor; zinc finger
 SUMMARY #length 468 #molecular_weight 52347 #checksum 3890
 DB 10; Score 1932; Match 64.6%; QryMatch 53.5%; Pred. No. 4.42e-254;
 Matches 245; Conservative 79; Mismatches 53; Indels 2; Gaps 2;
 DB 91 despsalniedrcigdkasgphyvhacegckoffrrtirkhlyvdckdrskdkntk 150
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 117 EEPNSLMAIECRVCGDKASGHYVHACEGCKFFRTIRLKLYVDRCDLNCRHKSR 176
 DB 151 nkcqycrfhcklsvgmshnairgmpseakakkaeilctehdksetadlks1gk1 210
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 Qy 177 NKCQICRFQKCLAVGMNSHAIERGRMPQAEEKKLAEI-SSDIDQNPESADRAAKHL 235
 DB 211 heaylnfmnkvhavrilagtnsnppfvihdneltcmaktlvkmvngved-keae 269
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 236 YDYSYKSPFLTKARALITGTTDKSFVIIYDNLSSLMGDKTKEKHTPDLQESEVA 295
 DB 270 vrfhhccqmsvetvlefakaiqfanldndqvtllkygresaiftmsslankdkg 329
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 296 IRIFQCCQRSVEAVQETEAKS1PGEVNLDLNDQVTLKYGVHEIYTMLSLANKDG 355
 DB 330 mliayngftrfknlrkpfcimepkfdfanfnalddedislfvaaiicgdrp 389
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 356 VLTSEQGMTRFLKSRLRKGDFMEPKFEEFKVFNALDDIAIFAVILSGDRP 415
 DB 390 qllniqyielqeqivhvlkhlgnsnhpdtdflfpkl1qknvdrlqlvtehqglqvikk 449
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 416 GLANVKP1IEDQDNLQALEQKLHNPESSQFLAKLJQMTDLRQIVTEVQLVQVTK 475
 DB 450 tesdaahp1qeiyrday 468
 ::|:|:|:|:|:|:|:
 Qy 476 TETDMSLPLQLEIYKDY 494
 DB 330 mliayngftrfknlrkpfcimepkfdfanfnalddedislfvaaiicgdrp 389
 ::|:|:|:|:|:|:|:|:|:|:|:|:|:
 Qy 356 VLISEQGMTRFLKSRLRKGDFMEPKFEEFKVFNALDDIAIFAVILSGDRP 415
 DB 390 qllniqyielqeqivhvlkhlgnsnhpdtdflfpkl1qknvdrlqlvtehqglqvikk 449
 ::|:|:|:|:|:|:|:|:|:|:
 Qy 416 GLANVKP1IEDQDNLQALEQKLHNPESSQFLAKLJQMTDLRQIVTEVQLVQVTK 475
 DB 450 tesdaahp1qeiyrday 468
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 Qy 476 TETDMSLPLQLEIYKDY 494
 RESULT 9 A65288 #type complete
 ENTRY peroxisome proliferator-activated receptor - rat
 TITLE #formal name Rattus norvegicus #common name Norway rat
 ORGANISM 2-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
 DATE 27-Jun-1994

ACCESSIONS A45288
 REFERENCE Geitlicher, M.; Widmark, E.; Li, Q.; Gustafsson, J.A.
 #authors Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4653-4657
 #journal Fatty acids activate a chimera of the clofibric
 #title acid-activated receptor and the glucocorticoid receptor.
 #accession A45288
 #status preliminary
 #molecule_type mRNA
 #residues 1-468 #label GOE
 #cross-references GB:M88592
 SUMMARY #length 468 #molecular_weight 52377 #checksum 4509
 DB 10; Score 1930; Match 65.2%; QryMatch 53.4%; Pred. No. 8.69e-254;
 Matches 247; Conservative 76; Mismatches 53; Indels 3; Gaps 3;
 DB 92 espgnal-niecringdkasgphyvhacegckffrtirkhlyvdckdrskdkntk 150
 ::|:|:|:|:|:|:|:|:|:|:
 Qy 117 EEPNSLMAIECRVCGDKASGHYVHACEGCKFFRTIRLKLYVDRCDLNCRHKSR 176
 DB 151 nkcqycrfhcklsvgmshnairgmpseakakkaeilctehdksetadlks1gk1 210
 |||||:||||:||||:||||:||||:||||:||||:||||:
 Qy 177 NKCQICRFQKCLAVGMNSHAIERGRMPQAEEKKLAEI-SSDIDQNPESADRAAKHL 235
 DB 211 heaylnfmnkvhavrilagtnsnppfvihdneltcmaktlvkmvngved-keae 269
 ::|:|:|:|:|:|:|:|:
 Qy 236 YDYSYKSPFLTKARALITGTTDKSFVIIYDNLSSLMGDKTKEKHTPDLQESEVA 295
 DB 270 vrfhhccqmsvetvlefakaiqfanldndqvtllkygresaiftmsslankdkg 329
 ::|:|:|:|:|:|:
 DB 330 mliayngftrfknlrkpfcimepkfdfanfnalddedislfvaaiicgdrp 389
 ::|:|:|:|:|:
 Qy 356 VLTSEQGMTRFLKSRLRKGDFMEPKFEEFKVFNALDDIAIFAVILSGDRP 415
 DB 390 qllniqyielqeqivhvlkhlgnsnhpdtdflfpkl1qknvdrlqlvtehqglqvikk 449
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 Qy 416 GLANVKP1IEDQDNLQALEQKLHNPESSQFLAKLJQMTDLRQIVTEVQLVQVTK 475
 DB 450 tesdaahp1qeiyrday 468
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 Qy 476 TETDMSLPLQLEIYKDY 494
 RESULT 10 A45360 #type complete
 ENTRY steroid hormone receptor NuC1 - human
 TITLE #common name man
 ORGANISM #sequence_revision 18-Nov-1994 #text_change
 DATE 10-Jun-1993
 ACCESSIONS A45360
 REFERENCE A45360
 #authors Rodan, C.A.
 #journal Mol. Endocrinol. (1992) 6:1634-1641
 #title Identification of a new member of the steroid hormone
 receptor superfamily that is activated by a peroxisome
 proliferator and fatty acids.
 #cross-references MUID:93078197
 #accession A45360
 #status preliminary; not compared with conceptual translation
 #molecule_type nucleic acid
 #residues 1-441 #label SCH

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Search completed: Fri Nov 17 08:31:34 1995
Job time : 24 secs.

CC	See also R13792-R13794.
SQ	Sequence 1237 AA;
DB 3;	Score 680; Match 33.3%; QryMatch 18.8%; Pred. No. 1.22e-43; Matches 120; Conservative 93; Mismatches 130; Indels 17; Gaps 15;
Db	242 tvcpeqddasgfhgvhsseggkffrrtisqkqkayrpotknqqsilrinrcqc 301 :: : : : : : : : : : : : : : : Qy 125 AIECRVCDASGKPHGTHAEGKGFFRTRIKLYDRC--DLNCRINKKSRSNCQCYC 182
Db	302 rkiclavasrdarfrgrpkrekrlaamqst-q-nr-qgq-palatel-ddapr1 366 : : : : : : : : : : : : : Qy 183 RFQKCLAVGASHNAIRGRMPQKAQKEKLLAEISSDDIQDLMPEASDLRALAKHLYDSYIKS 242
Db	357 la-avlrrahletctfekvs-aanqrardpsysmptl-lacoplnpapelqseqefsq- 412 :: : : : : : : : : : : Qy 243 FPLTKAKARALITGKTIDKSFPEFVYDONSIMMEDKIKFKHTPLQEQSKEVAIRFQGCC 302
Db	413 pfahv--irgvifdampqfqlltqaddkfclklaglfadlfvliimfdssinsicln 470 : : : : : : : : : Qy 303 QFRSEVAQETTEYAKSIPGIVNLDLQDTVLKYGWHEIIYTMPLASLANKD-GVILS-E 360
Db	471 qgv-mrrdaingana-qf1vdstfnfaermmsmltdaeiglfcaviltpdrpgml 528 : : : : : : : : Qy 361 GQGEMTREFLKSRLKPKFCDFMEPKFEPFKENALEDDSDIAFLAVIILSGDRPGLINV 420
Db	529 eliekavysrlqglqyiraqaprdqeqflaklletmpdlrtstlhtekuvfrtchke1 588 : : : : : : : Qy 421 KPIEDQNLQALEQIKINHPESSQLFAKLQKMTDLRQIVTEHVQLLQVIKKTETDM 480
RESULT 4	ID P80921 standard; protein; 456 AA. AC P80921; DT 29-DEC-1990 (first entry) DE Sequence encoded by human placenta thyroid receptor c-erbA cDNA KW Hormone receptor; hormone-binding; transcription activation. OS Homo sapiens. PN W0803168-A. PD 05-MAY-1988. PF 23-OCT-1987; U02782. PR 20-OCT-1987; US-108471. PA (SALK) Salk Inst for Biol Stud. PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V; DR WPI; 88-133242/19. DR N-PSDB; N80923. PT Recombinant DNA encoding hormone receptors - comprising glucocorticoid, mineralocorticoid, thyroid hormone and novel hormone receptors PT and novel hormone receptors PS Example: Fig VTI-1(B); 243pp; English. CC DNAs encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpd.s for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic assays. CC Sequence - 410 AA;
DB 2;	Score 510; Match 30.7%; QryMatch 14.1%; Pred. No. 5.61e-30; Matches 115; Conservative 96; Mismatches 137; Indels 26; Gaps 25;
SQ	Sequence 456 AA; DB 102 cvvegdkatghyrcitgegkcgkffrrtqkqnlhpssckvegcvcidkvtrngcqecrf 161 : : : : : : : : Qy 128 CRVCDASGKPHGTHAEGKGFFRTRIKLYDRC--DLNCRINKKSRSNCQCYC 184
Db	162 kkcivymadlv-1ddskrakrkiae-ne-kr-r-reelq-kgs-hkeptdeew 215 : : : Qy 185 QKCLAVGASHNAIRGRMPQAEKELIAEISSDDIQDLMPEASDLRALAKHLYDSYIKSFP 244
Db	216 likltceahratnaq-shw-k-qkpkfl-ped-igapiivnspgkq-vdlaef-s-hf 267 : : Qy 245 LTKAKARALITGKTIDKSFPEFVYDONSIMMEDKIKFKHTPLQEQSKEVAIRFQGCCF 304
Db	268 tkittpaairrvdfakkpfcelpedqkll-kccameimsrlraavydposetitln 326 : : Qy 305 -RSVE-AQGTTETYAKSIPGIVNLDLQDTVLKYGWHEIIYTMPLASLNMKG-QWLE 360
Db	327 gemavirgqqln--ggqvvsraidaflqmslfnllddtetalqavlmssdrplacy 384 : : Qy 361 GQGEMTREFLKSRLKPKFCDFMEPKFEPFKENALEDDSDIAFLAVIILSGDRPGLINV 420
RESULT 5	ID P80936 standard; protein; 410 AA. AC P80936; DT 29-DEC-1990 (first entry) DE Sequence encode by thyroid hormone receptor cdNA from rat brain clone DE rbeA12. KW Hormone receptor; hormone-binding; transcription activation. OS Rat; PN W0803168-A. PD 05-MAY-1988. PF 23-OCT-1987; U02782. PR 20-OCT-1987; US-108471. PA (SALK) Salk Inst for Biol Stud. PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V; DR WPI; 88-133242/19. DR N-PSDB; N80923. PT Recombinant DNA encoding hormone receptors - comprising glucocorticoid, mineralocorticoid, thyroid hormone and novel hormone receptors PT and novel hormone receptors PS Example: Fig VTI-1(B); 243pp; English. CC DNAs encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpd.s for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic assays. CC Sequence - 410 AA;
DB 2;	Score 510; Match 30.7%; QryMatch 14.1%; Pred. No. 5.61e-30; Matches 115; Conservative 96; Mismatches 137; Indels 26; Gaps 25;
SQ	Sequence 456 AA; Db 52 qvvvqgdaktyhyrcitgegkffrrtqkqnlhpssckvegcvcidkvtrngcqecrf 111 : : Qy 127 EGRCGDASGFHGVHAEGCKGFFRTRIKLYDRC--DLNCRINKKSRSNCQCYC 183
Db	112 fkkciavymadlv-1ddskrakrkiae-ne-kr-k-em-irs1qlgrp-ep-tpew 165 : : Qy 184 FKCLAVGASHNAIRGRMPQAEKELIAEISSDDIQDLMPEASDLRALAKHLYDSYIKSFP 243
Db	166 dlihv-ateahrstrnqshs-k-qrkpkfl-pd-dqspivsmpdgdk-vdleaf-s-e 217

Qy	244	PJTKKARAILTGKTIDKSPFVYDNNLSMMEDDKIKFKHTPLQESEKVAIRFGCQ	303
Db	218	ftkittpafrvdfakkpmfsepcqdkllk-gccmeimslraavrydpdsdtltl	276
Qy	304	F-RSVE-AVQELTEVAKSPGTVNLDLQDQFLKQGYTHEIYTIALSM-NKG-VLIS	359
Db	277	sgemtvrkqklkn-gglygysdafeigksisafnlldtevalqavlmstsgllc	334
Qy	360	EGCGFTRREFEALSLRKPFDFMEPKPEFAKENAELDDSDIAFEIAVILSGDRGLIN	419
Db	335	vdkieksgayllafetehymvhnrkhnhphfwpklnkvtalrnigachaeरfhlkmvecept	394
Qy	420	VKPIEDDNLLQALEQKLHNPESSOLFALKLORMTDLRQIVTEHV-QLIQUIKTTET	478
Db	395	el-fppfllevedf 407	
Qy	479	DMSLHPLQEIYRD 492	
RESULT			
ID	6	RAT7621 standard; Protein; 514 AA.	
AC		AC R47621;	
DT	07-JUL-1994	(first entry)	
DE		Rat thyroid hormone receptor.	
KW		Pituitary-specific thyroid hormone receptor; PTHRH; erbA gene; hypothyroidism; hyperthyroidism.	
KW		Rattus sp.	
OS		US5284999-A.	
PN		08-FEB-1994	
PD		05-APR-1990	504806.
PF		05-APR-1990	US-504806.
PR		13-MAY-1993	US-069643.
PR		(BGHM) BRIGHAM & WOMENS HOSPITAL.	
PA		PA	
PI		Chin WW, Hodin RA, Lazar MA,	
DR		WPI; 94-056439/07.	
DR		P-PSDB; Q54086.	
PT		Recombinant DNA molecule encodes pituitary-specific thyroid hormone receptor - useful for therapy of e.g. hypo- and hyper-thyroidism	
PT		Disclosure; Column 21-22; 12pp; English.	
PS		A rat GH3 cell cDNA library was screened with rat erbA sequences to isolate a gene encoding PTHRH. The sequence of the full-length cDNA for PTHRH is given in Q54086, and the deduced amino acid sequence in R47621.	
SQ		Sequence 514 AA;	
DB	8	Score 501; Match 31.1%; QryMatch 13.9%; Pred. No. 2.92e-2	
Matches	116;	Conservative 101; Mismatches 130; Indels 26; Gaps 1	
Db	160	cvcgdkatgyhycitecgokffrrrtiqkhspscyekgckidkvtrngcqceqr	219
Qy	128	CRVGDAASGEHYGVHACEGKGFERRTI-R-IKLYD-RCDLNCRHKRSRNKQYCRF	184
Db	220	kkcijvgmadv-llddskrlakkkiee-nrq-kr-rreelq-ksig-hkpeptdeew	273
Qy	115	: ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;	
Db	274	liktevahatnag-ssh-w-k-qrkf1-ped-icqapimapegk-vdleaf-s-hf	325
Qy	245	LTKKARAILTGKTIDKSPFVYDNNLSMMEDDKIKFKHTPLQESEKVAIRFGCQF	304
Db	326	tkittpafrvdfakkpmfsepcqdkllk-gccmeimslraavrydpdsdtltl	384

RESULT 8
 ID R27533 standard; Protein; 797 AA.
 AC R27533;
 DT 09-MAR-1993 (first entry)
 DE myl/RAR-alpha fusion.
 KW Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia;
 KW t(15;17) translocation; chromosome 15; chromosome 17; PCR; primer;
 KW synthetic.
 OS WO9216660-A.
 PN 01-OCT-1992.
 PD 23-MAR-1992; U02320.
 PR 22-MAR-1991; US-673838.
 PA (SLOC) SLOAN KETTERING INST CANCER.
 PI Dmitrovsky E, Evans RM, Frankel S, Kazizuka A, Miller WH,
 Warrell RP;
 PI WO92-349240/42.
 DR N-PDB; Q3934.
 PT Marker for acute promyelocytic leukaemia and other neoplasias -
 PT comprising nucleic acid and encoded abnormal retinoic acid
 PT receptor-alpha receptor
 PS Disclosure; Fig 4; 84pp; English.
 CC The sequence given shows a fusion between retinoic acid receptor
 CC (RAR)-alpha and myl which is characteristic of acute promyelocytic
 CC leukemia (APL). This is caused by a translocation of a portion of
 CC the long arm of chromosome 17 onto the long arm of chromosome 15
 CC (t(15;17) (q21;q11-22)). The breakpoint region has been cloned and it
 CC has been shown that DNA rearrangements are clustered in the region
 CC of the first intron of RAR-alpha. This sequence was isolated by
 CC polymerase chain reaction (PCR) using primers which correspond to
 CC sequences both 5' and 3' to the breakpoint region.
 SQ Sequence 797 AA;

DB 5; Score 472; Match 31.8%; QryMatch 13.1%; Pred. No. 5.87e-27;
 Matches 130; Conservative 100; Mismatches 131; Indels 42; Gaps 23;

Db 379 fkvrldscitqghaietqssseelvpspsppplprykpfcvqdksayhygvs 438
 Qy 84 YDQKLEYSAKVEFASPYTSETQLYNPKHEEPSNSLMAICRVDKASEFHGVH 143

Db 439 acegcgkfrriqkmuytchrdnkciinktrnrcyqlqkfcvngmkesvndr- 497
 Qy 144 ACEGCKGFRRTRILYD-RCDINCRTHRSRNKCYCFCQKCLAVGMHNARFGRM 202

Db 498 nkkkkvppe-ccseytttpevg---iek-vrhkgetfp---alcq---1-gk---- 542
 Qy 203 PQAEKEKLAEIISDIDQINPESADIRALAKLYDSYIKSFPLIKARAILTKTDKS 262

Db 543 -ytt-n-nas---seqrvsl-did-lwdkfslselstk---efaklgp 583
 Qy 263 PFTVYDMSLMMGEDRIKFRHTDQSKEVATIRIFQQCFRSYEAVQEITEAKSIPG 322

Db 584 fttltiadqtlkaacldilrlirctrytpedqmtfsdglt-1nrtqmhma--gfqpl 640

RESULT 9
 ID R33744 standard; Protein; 440 AA.
 AC R33744;
 DT 23-JUL-1993 (first entry)
 DE XR2.
 KW Receptor; XR2; DNA binding domain; human; retinoic acid receptor-alpha;
 KW hRAR-alpha; thyroid receptor-beta; hTR-beta; glucocorticoid receptor;
 KW hGR; retinoid X receptor-alpha; hRXR-alpha; verhr3; verhr5; ligand;
 KW transcription-activation; response element.
 OS Homo sapiens.
 PN WO9306215-A.
 PD 01-APR-1993.
 PR 08-SEP-1992; U07570.
 PR 17-SEP-1991; US-761068.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 PI Borgmeyer UK, Evans RM, Giguere V, Mangelsdorf DJ;
 PI Oto AE, Yao TP;
 DR WO93-117536/14.
 DR N-PDB; Q39088.
 PT DNA encoding proteins of thyroid-steroid hormone receptor
 PT super-family - useful for screening for agonists-antagonists of
 PT such receptors
 PS Claim 9; Page 40-42; 71PP; English.
 CC This sequence represents the receptor XR2. This polypeptide has a
 CC DNA binding domain comprising approx. 55% amino acid sequence identity
 CC with the DNA binding domain of human retinoic acid receptor-alpha
 CC (hRAR-alpha), about 56% amino acid sequence identity with the DNA
 CC binding domain of human thyroid receptor-beta (hTR-beta), about 50%
 CC amino acid sequence identity with the DNA binding domain of human
 CC glucocorticoid receptor (hGR) and about 52% amino acid sequence
 CC identity with the DNA binding domain of human retinoid X receptor-
 CC alpha (hRXR-alpha). XR2 receptor can be used for testing a compound
 CC for its ability to regulate transcription-activating effects of a
 CC receptor polypeptide, identifying compounds which act as ligands for
 CC the receptor polypeptides and for identifying response elements for
 CC the receptor polypeptides.
 SQ Sequence 440 AA;

DB 6; Score 471; Match 28.3%; QryMatch 13.0%; Pred. No. 7.05e-21;
 Matches 108; Conservative 100; Mismatches 141; Indels 26; Gaps 22;

Db 76 krkkgapkpkngnelecsqcdkasgfhynvlscdgckgfffrsrsvkgahiyichsgggchpm 135
 Qy 114 KRHEEPNSLMAIE-CRVCGDASGPHYVHCEGKGFSFRRTIRIKLJYD-RCDLNCR 171

Db 136 dymrrkrcgecpkrlkrqagtmcreev---lse-eqirl-kklkrqee-qahatsl-p- 186
 Qy 172 HKTSRKQCRFQKCLAVGMHSNAFRGRMQAEKEKLAEIISDIDQINPESADIRAL 231

Db 187 prssppaqip-qlspeql-gml-ekiva-aq-qqcnrsfs-dr-irvtpwmap-dphs 239
 Qy 232 AKHLYDSYIKSFPLIKARAILTQKTTDKSPTVYDMSLMMGEDRIKFRHTDQS 291

Db	240 reargrfahftel-aivsgveifvdafqkpgflqlsredgiallktsaevmllettst 298	Db	201 -alcq--l-gk-----ytc-n-ns---seqls-did-lwfslstk---c-i-- 236
Qy	292 KEVAIRIFQCQFRSVZAVETEYAKSTPGFVNLDINDQVTLKYGVHEIYTMLASI, 350	Qy	247 KAKARALLIGKTKTDESPVITDMSLAMGEDKIFKFHTPLQESSEKEVARIFQGCFRS 306
Db	299 ynpasesitfilksfsynredfaka-giqv-efinpfesramelqindaefalliai 356	Db	237 iktv---efakqkqffltiaditllkacldlilirctrypeqdmtfsdglt- 291
Qy	351 WAKDGWLISEGGFEN-TFLKSIRKPFAVKNALEDDSDAIFIATIAMI 408	Qy	307 VEAVQITEYAKSTPGFVNLDINDQVTLKYGVHEIYTML-ASLM-NKGVLISSEQGF 364
Db	357 ifsdadpnyqddlqverlqhtyealhaywstihphdrlnfpmlmklvrltssvhse 416	Db	292 lntqmhma-qfppltdlvfanqlplmedaetglsaisciaicqdrdqleqpordv 349
Qy	409 ILSDRPGILANVKPTEDIQDNILQALEQIKINHPESSQLFAKLLQRMTDLROIVTEHQ 468	Db	365 MTRFLKSURKEFGDFMEPKFPEFKVNALELDSSDAIFIATIAMI 424
Db	417 --qvfafrlqdklppllsei 435	Db	350 mlqepyleakkyvkvkrpsphmpfpmnkmtdrsisakgaervitlkm-eipgamp 408
Qy	469 LIQVIRKTETDMSLPLQEI 489	Qy	425 DQDNLQLELQIKLNHPESSQLFAKLLQRMTDLROIVTEHQVLLQVIRKTTEDMSLHP 484
Db	RESULT 10	Db	409 liqem 413
ID	R27534 standard; Protein; 462 AA.	Qy	485 LIQEI 489
AC	R27534;	RESULT 11	
DT	09-MAR-1993 (first entry)	ID	R10547 standard; protein; 462 AA.
DE	RAR-alpha protein.	AC	R10547;
KW	Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia;	DT	11-APR-1991 (first entry)
KW	APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15;17) (q21;q11-22)]; breakpoint; polymerase chain reaction.	FT	Murine Retinoic Acid Receptor-alpha (deduced from cDNA).
KW	Synthetic.	DE	mouse; retinoic acid receptor; mRAR-alpha; embryogenesis.
OS	PN W09216660-A.	KW	
PN	01-OCT-1992.	OS	Mus musculus.
PD	PF 23-MAR-1992; U02320.	FH	Key
PR	PR 22-MAR-1991; US-673838.	Region	Location/qualifiers
PR	PR 22-MAR-1991; US-675084.	Region	1..59
PA	(SLOK) SLOAN KETTERING INST CANCER.	Label= Region A	
PT	Marker for acute promyelocytic leukemia and other neoplasias - comprising nucleic acid and encoded abnormal retinoic acid PT receptor-alpha receptor	Label= Region B	
PT	Disclosure; Page 43-46; 84pp; English.	Label= Region C	
PS	The sequence given represents the amino acid sequence of the retinoic acid receptor (RAR)-alpha protein. The gene encoding this protein is disrupted in a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [t(15;17) (q21;q11-22)]. This causes a fusion RAR-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). The breakpoint region has been cloned and it has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR). The primers used for amplification of this sequence can also be used to amplify the translocated region.	Label= Region D	
CC	Sequence 462 AA;	note= "important for differential trans-activation by other nuclear receptors"	
CC	Sequence 462 AA;	Region	88..153
CC	Sequence 462 AA;	Label= Region E	
CC	Sequence 462 AA;	note= "DNA binding domain. 95 per cent amino acid identity between mRAR's"	
CC	Sequence 462 AA;	Region	154..199
CC	Sequence 462 AA;	Label= Region F	
CC	Sequence 462 AA;	note= "putative hinge region"	
CC	Sequence 462 AA;	Region	200..419
CC	Sequence 462 AA;	Label= Region G	
CC	Sequence 462 AA;	note= "ligand binding domain"	
CC	Sequence 462 AA;	Region	420..462
CC	Sequence 462 AA;	Label= Region H	
CC	Sequence 462 AA;	note= "well conserved between mRAR's"	
CC	Sequence 462 AA;	Region	PD 06-FEB-1991.
CC	Sequence 462 AA;	Label= Region I	PD 06-FEB-1991.
CC	Sequence 462 AA;	note= "putative hinge region"	PF 29-JUN-1990; 112469.
CC	Sequence 462 AA;	Region	PR 30-JUN-1988; US-374690.
CC	Sequence 462 AA;	Label= Region J	PR 29-MAR-1990; US-302140.
CC	Sequence 462 AA;	note= "putative hinge region"	(INRM) INSERM INST NAT SANTE.
CC	Sequence 462 AA;	Region	PA (SQU1) LES LABS SQUIBB SA.
CC	Sequence 462 AA;	Label= Region K	PA Champon P, Kastner P, Krust A, Petkovich M, Zelent A;
CC	Sequence 462 AA;	note= "putative hinge region"	PI Leroy P, Mandelsoh C, Staub A;
CC	Sequence 462 AA;	Region	DR 91-038271/06.
CC	Sequence 462 AA;	Label= Region L	PT Novel human and mouse retinoic acid receptors - encode proteins used to assay for agonists and antagonists
CC	Sequence 462 AA;	note= "putative hinge region"	PS Disclosure; Fig 1; 33pp; English.
CC	Sequence 462 AA;	Region	CC An 11.5 day-old total mouse embryo lambda gt10 cDNA library was screened with labelled human RAR-alpha probes. Positive clones were isolated, mapped and sequenced. A set of mRAR-alpha clones was

Db 81 cfcgdkassghygsacecgkffrissqkmuytchrkneinkvtmrccyrlqk 140
 Qy 128 CRVCGDKASGFHYGVHAEGCKGFFRKTRIKLYD-RCDLNCRHKSRSRNKQYCFRQK 186
 Db 141 cfevomskesvndr-nkkketskqe-ctsesmtaeldl-t-ek-irkahqetfp-s 194
 Qy 187 CLAVGMSHNARFRGMPQAEEKEKLLAEISSDIDOLNPESADILAKLKHLYDSYTKSFPLT 246
 Db 195 -1-cq-1-gk-----ytts--sadhvr1-dlg-lwdkfseatt---c--- 228
 Qy 247 KAKARAILTGTKTDSPPVIVDMNSLAMGEDKIKFRHTIPLOQESKEVARIFQGQQFRS 306
 Db 229 i-ik-ivefakrlpgftgliaadqtlkaacdldilirictrypeqdttfsdglt- 284
 Qy 307 VENQETEYAKSPGPFWNLINDQVTLKYXWHEIYTML-ASLM-NKDGVLISSEQF 364
 Db 285 Inrtqmhma--gfpltlalvftfanganlpemddtgllsalicgqdgleptkvd 342
 Qy 365 MTERFLKLRRPFGDFMEPKFEFAVKENALEDDSDLAIFIATLISGDRGLINKPTE 424
 Db 343 klaplpleakiyirkrpskphmfkilmktlrsisakgaervitlkm-eipgmp 401
 Qy 425 DIQDNLQALELQKINHPESSOLFALKQKMDLIRQIVTEHQVLLQVIKKTTDMSLHP 484
 Db 402 liqem 406
 Qy 485 LIQEI 489

RESULT 14

ID R55128 standard; Protein; 448 AA.

AC R55128;

DT 11-JAN-1995 (first entry)

DE Retinoic acid receptor RA-beta.

KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone;

KW hepatoma; retinoid; antibody.

OS Homo sapiens.

PN US5317090-A.

PD 31-MAY-1994.

PF 16-DEC-1987; 133687.

PR 16-DEC-1987; US-133387.

PR 17-DEC-1987; US-134130.

PR 20-JUN-1988; US-209009.

PR 30-NOV-1988; US-278136.

PR 30-MAR-1989; US-330405.

PR 21-AUG-1991; US-751612.

PR 30-MAR-1992; US-860577.

PR 11-DEC-1992; US-989302.

PA (INSP) INST PASTEUR,

PI Brand N, Chambon P, De THE HB, Dejean A, Krust A;

PI Marchio A, Petkovich M, Tiollais P;

DR WP1; 94-17633/21.

DR N-PSDB; R55128.

PT Antibody specific for retinoic acid receptor-beta - useful for detecting, quantifying and identifying agonists and antagonists PT of retinoid activity.

PS Claim 1; Figure 2; 35pp; English.

CC The retinoic acid receptor is encoded by a gene designated hap. The CC hap gene is transcribed at low level in most human tissues, but the CC gene is overexpressed in prostate and kidney. Six out of seven CC hepatoma or hepatoma-derived cell lines express a small hap transcript which is undetectable in normal adult and foetal livers CC but present in all non-hepatic tissues tested.

SQ Sequence 448 AA;

Db 10; Score 457; Match 32.9%; QryMatch 12.6%; Pred. No. 9.05e-26; Matches 120; Conservative 92; Mismatches 111; Indels 42; Gaps 24;

Db 81 cfvcgdkassghygsacecgkffrissqkmuytchpkvinkvtmrccyrlqk 140
 Qy 128 CRVCGDKASGFHYGVHAEGCKGFFRKTRIKLYD-RCDLNCRHKSRSRNKQYCFRQK 186

Db 141 cfevqmskesvndr-nkkketskqe-ctsesmtaeldl-t-ek-irkahqetfp-s 194
 Qy 187 CLAVGMSHNARFRGMPQAEEKEKLLAEISSDIDOLNPESADILAKLKHLYDSYTKSFPLT 246

Db 195 -1-cq-1-gk-----ytts--sadhvr1-dlg-lwdkfseatt---cik- 228
 Qy 247 KAKARAILTGTKTDSPPVIVDMNSLAMGEDKIKFRHTIPLOQESKEVARIFQGQFRS 306

Db 195 -1-cq-1-gk-----ytts--sadhvr1-dlg-lwdkfseatt---cik- 231
 Qy 247 KAKARAILTGTKTDSPPVIVDMNSLAMGEDKIKFRHTIPLOQESKEVARIFQGQFRS 306

Db 195 -1-cq-1-gk-----ytts--sadhvr1-dlg-lwdkfseatt---cik- 231
 Qy 247 KAKARAILTGTKTDSPPVIVDMNSLAMGEDKIKFRHTIPLOQESKEVARIFQGQFRS 306

Db 232 i-vq----fakrlqfqltglatdqtllkaacdldilirictrypeqdtmtfsdlt- 284
 Qy 307 VENQETEYAKSPGPFWNLINDQVTLKYXWHEIYTML-ASLM-NKDGVLISSEQF 364

Db 232 i-vq----fakrlqfqltglatdqtllkaacdldilirictrypeqdtmtfsdlt- 284
 Qy 307 VENQETEYAKSPGPFWNLINDQVTLKYXWHEIYTML-ASLM-NKDGVLISSEQF 364

Db 285 lmrtqmhma-qfgpltdlvftfanqlplmddtqfqlsaiclgdrqdrqleptkv 342
 Qy 365 MTERFLKLRRPFGDFMEPKFEFAVKENALEDDSDLAIFIATLISGDRGLINKPTE 424

Db 285 lmrtqmhma-qfgpltdlvftfanqlplmddtqfqlsaiclgdrqdrqleptkv 342
 Qy 365 MTERFLKLRRPFGDFMEPKFEFAVKENALEDDSDLAIFIATLISGDRGLINKPTE 424

Db 343 klqepplleakiyirkrpskphmfkilmktlrsisakgaervitlkm-eipgmp 401
 Qy 425 DIQDNLQALELQKINHPESSOLFALKQKMDLIRQIVTEHQVLLQVIKKTTDMSLHP 484

Db 402 liqem 406
 Qy 425 DIQDNLQALELQKINHPESSOLFALKQKMDLIRQIVTEHQVLLQVIKKTTDMSLHP 484

Db 402 liqem 406
 Qy 485 LIQEI 489

RESULT 15
 ID R10348 standard; Protein; 448 AA.
 AC R10348;
 DT 11-APR-1991 (first entry)
 DE Murine Retinoic Acid Receptor-beta (deduced from cDNA).
 KW mouse; retinoic acid receptor; mRAR-beta; embryogenesis.
 OS Mus musculus.
 FH Key
 FT Region 1..52
 FT /label= Region A
 FT /note= "important for trans-activation by other nuclear receptors"
 FT Region 53..80
 FT /label= Region B
 FT /note= "well conserved between mRAR's"
 FT Region 81..146
 FT /label= Region C
 FT /note= "DNA binding domain, 95 per cent amino acid identity between mRAR's"
 FT Region 147..192
 FT /label= Region D
 FT /note= "putative hinge region"
 FT Region 193..412
 FT /label= Region E
 FT /note= "ligand-binding domain"
 FT Region 413..448
 FT /label= Region F
 PN EP-411323-A.
 PD 06-FEB-1991.
 PF 29-JUN-1990; 112469.
 PR 30-JUN-1989; US-31469.

PR 29-MAR-1990; US-502140.
 PA (INRM) INSERM INST NAT SANTE.
 PA (SOUTI) LES LABS SQUIBB SA.
 PI Chambon P, Kastner P, Krust A, Petkovich M, Zelent A;
 PI Leroy P, Mendelsoh C, Staub A;
 PI RPI ; 91-038271/06.
 DR Novel human and mouse retinoid acid receptors - encode proteins
 PT used to assay for agonists and antagonists
 PS Disclosure; Fig 1; 33pp; English.
 CC An 11.5 day-old total mouse embryo lambda gt10 cDNA library was
 screened with labelled humanRAR-beta probes. Positive clones were
 CC isolated, mapped and sequenced. A set of mRAR-beta clones was
 CC identified on the basis of a 98 percent homology of their cDNA.
 CC deduced amino acid sequence with that of human RAR-beta. There are
 CC 8 amino acid substitutions (mostly conservative) between the human
 CC and mouse sequences. See also R10547, Q10388-9 and Q10405-8.
 SQ Sequence 448 AA;

DB	Score	Match	Mismatches	Pred.	No.	Length
DB	2;	456;	Match 32.9%; QryMatch 12.6%;	Pred.	No.	1.09e-25;
Matches	120;	Conservative	91;	Mismatches	112;	Indels 42;
						Gaps 24;
Db	81	cfcvcdksssghygvsacecgkfrsrqckumiytchrdknvcinkvtrncqyrlqk	140			
Qy	128	CRVCGDKASFRHYGVHACECKGFFRRTIRKLIVD-RCDLNCRHCKSRNCQYCREFQK	186			
Db	141	cfcvqmskeevrndr-nkkkkepskge-ctesyeantaelldl-t-ek-irkahgetfp-s	194			
Qy	187	CLAVGMSRNATRGRMEQAKZERLLEISSDIDQNPESADRAKHLHDYOSYIKSFPLT	246			
Db	195	-1-cq--1-qk-----ytns--sadrtrrl-dlq-lwdkfslatk---c---	228			
Qy	247	KAKARALITERTTDKSPFVYDANSIMMGEDKIKFKHITPLQEQSKVEAIRFQGGQFRS	306			
Db	229	i-ik-ivefaekrpgtgtitadqtlLikaacdLiliirictrypegdttfsegt-	284			
Qy	301	VEAVQEITEYAKS1PQGFVNLDQVTLKYGYHEIYTML-ASLM-NFDGVILISEGGCF	364			
Db	285	Inrtqmhma--ggplcdlvftfanqlplemdttglisaicLcgdrqdeleptkv	342			
Qy	305	MTREFLAKSLRKXPECDFMEPKREFAVKENAELDDSDIAIFIAVIILSGDRPGILNKPIE	424			
Db	343	kicpbleakhiyirktrpsphmfplmktdlrsisakgervitlkm-eiposapp	401			
Qy	425	DIONNLQALEQKUMLAHPESSQFLAKLQMDLROIVTEHWQLQVIKKETDMSLHP	484			
Db	402	Liqem 406				
Qy	485	LQEI 489				